SEQUENCE LISTING

<110> ROSSI, EDMUND A.
      CHANG, CHIEN HSING
      MCBRIDE, WILLIAM J.

<120> POLYVALENT PROTEIN COMPLEX

<130> 41133-0006US1

<140> 10/829,388
<141> 2004-04-22

<150> 60/464,532
<151> 2003-04-22

<150> 60/525,391
<151> 2003-11-24

<160> 20

<170> PatentIn version 3.2

<210> 1
<211> 370
<212> PRT
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<220>
<223> Chimeric sequence from multiple species

<400> 1
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Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
            20   25   30

Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro
        35   40   45

Gly Lys Gly Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp
    50   55   60

Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
65   70   75   80

Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
                85   90   95

Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp
        100   105   110

Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser Gly Gly
        115   120   125

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
        130   135   140

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
145   150   155   160

Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
            165   170   175

Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg
        180   185   190

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
        195   200   205

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu
        210   215   220

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu
225   230   235   240

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
        245   250   255

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp
        260   265   270

Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
        275   280   285

Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr
        290   295   300

Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
305   310   315   320

Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly

```
              325                      330                      335

Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr
            340                  345              350


Trp Gly Gln Gly Thr Pro Val Thr Val Ser Val Asp His His His His
        355                  360              365


His His
    370


<210> 2
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric sequence from multiple species

<400> 2
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1               5                   10              15


Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
            20                  25              30


Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
        35                  40              45


Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val
    50                  55              60


Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65                  70              75                  80


Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln
                85                  90              95


Tyr Ser Leu Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105             110


Arg Gly Gly Gly Gln Phe Met Glu Val Gln Leu Val Glu Ser Gly Gly
        115                 120             125


Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser
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                130                        135                        140


    Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro
    145                 150                 155                 160


    Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr
                    165                 170                 175


    Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp
                    180                 185                 190


    Asn Ala Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
                195                 200                 205


    Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp
        210                 215                 220


    Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Gly Gly Gly
    225                 230                 235                 240


    Gly Ser Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ala Val Ser
                    245                 250                 255


    Pro Gly Glu Arg Val Thr Leu Thr Cys Lys Ser Ser Gln Ser Leu Phe
                    260                 265                 270


    Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro
                275                 280                 285


    Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser
        290                 295                 300


    Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    305                 310                 315                 320


    Leu Thr Ile Asn Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
                    325                 330                 335


    Thr Gln Val Tyr Tyr Leu Cys Thr Phe Gly Ala Gly Thr Lys Leu Glu
                340                 345                 350


    Leu Lys Arg Leu Asp His His His His His His
            355                 360
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<210> 3
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 3
gatcccctgc agggagctca ctagta                                            26


<210> 4
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized oligonucleotide

<400> 4
gatcccctgc agggagctca ctagta                                            26


<210> 5
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized oligonucleotide

<400> 5
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<210> 6
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized oligonucleotide

<400> 6
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<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized oligonucleotide
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<400> 7
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<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized oligonucleotide

<400> 8
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<210> 9
<211> 1110
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric sequence from multiple organisms

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atgtcttggc ttcgccagac tccgggaaag gggctggagt gggtcgcaac cctgagtggt   180

gatggtgatg acatctacta tccagacagt gtgaagggtc gattcaccat ctccagagac   240

aatgccaaga acagcctata tctgcagatg aacagtctaa gggctgagga cacggccttg   300

tattactgtg caagggtgcg acttggggac tgggacttcg atgtctgggg ccaagggacc   360

acggtctccg tctcctcagg aggtggcgga tccgacatcc agctgaccca gagcccaagc   420

agcctgagcg ccagcgtggg tgacagagtg accatcacct gtaaggccag tcaggatgtg   480

ggtacttctg tagcttggta ccagcagaag ccaggtaagg ctccaaagct gctgatctac   540

tggacatcca cccggcacac tggtgtgcca agcagattca gcggtagcgg tagcggtacc   600

gacttcacct tcaccatcag cagcctccag ccagaggaca tcgccaccta ctactgccag   660

caatatagcc tctatcggtc gttcggccaa gggaccaagg tggaaatcaa acgtctcgag   720

ggcggaggta gcgaggtcca actggtggag agcggtggag gtgttgtgca acctggccgg   780

tccctgcgcc tgtcctgctc cgcatctggc ttcgatttca ccacatattg gatgagttgg   840

gtgagacagg cacctggaaa aggtcttgag tggattggag aaattcatcc agatagcagt   900

acgattaact atgcgccgtc tctaaaggat agatttacaa tatcgcgaga caacgccaag   960
```

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aacacattgt tcctgcaaat ggacagcctg agacccgaag acaccggggt ctattttgt    1020

gcaagccttt acttcggctt cccctggttt gcttattggg gccaagggac cccggtcacc    1080

gtctccgtcg accatcatca tcatcatcat                                     1110
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<210> 10
<211> 1089
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric sequence from multiple organisms

<400> 10
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gtgggtgaca gagtgaccat cacctgtaag gccagtcagg atgtgggtac ttctgtagct    120

tggtaccagc agaagccagg taaggctcca aagctgctga tctactggac atccacccgg    180

cacactggtg tgccaagcag attcagcggt agcggtagcg gtaccgactt caccttcacc    240

atcagcagcc tccagccaga ggacatcgcc acctactact gccagcaata tagcctctat    300

cggtcgttcg gccaagggac caaggtggaa atcaaacgtg gaggtggcca attcatggag    360

gtccaactgg tggagagcgg tggaggtgtt gtgcaacctg gccggtccct gcgcctgtcc    420

tgctccgcat ctggcttcga tttcaccaca tattggatga gttgggtgag acaggcacct    480

ggaaaaggtc ttgagtggat tggagaaatt catccagata gcagtacgat taactatgcg    540

ccgtctctaa aggatagatt tacaatatcg cgagacaacg ccaagaacac attgttcctg    600

caaatggaca gcctgagacc cgaagacacc ggggtctatt tttgtgcaag cctttacttc    660

ggcttcccct ggtttgctta ttggggccaa gggacccggg tcaccgtctc cggaggcggt    720

ggatccgaca ttgtgatgac acaatctcca tcctccctgg ctgtgtcacc cggggagagg    780

gtcactctga cctgcaaatc cagtcagagt ctgttcaaca gtagaacccg aaagaactac    840

ttgggttggt accagcagaa accagggcag tctcctaaac ttctgatcta ctgggcatct    900

actcgggaat ctggggtccc tgatcgcttc tcaggcagtg gatccggaac agatttcact    960

ctcaccatca acagtctgca ggctgaagac gtggcagttt attactgcac tcaagtttat   1020

tatctgtgca cgttcggtgc tgggaccaag ctggagctga aacggctcga ccatcatcat   1080

catcatcat                                                           1089
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<210> 11

<211> 364
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric sequence from multiple species

<400> 11

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Met Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly
1               5                   10                  15

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile
            20                  25                  30

Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Val Ala Thr Leu Ser Gly Asp Gly Asp Asp Ile Tyr Tyr Pro Asp Ser
    50                  55                  60

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu
65                  70                  75                  80

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr
            85                  90                  95

Cys Ala Arg Val Arg Leu Gly Asp Trp Asp Phe Asp Val Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Ser Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln
        115                 120                 125

Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
    130                 135                 140

Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Ser Val Ala Trp
145                 150                 155                 160

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Thr
            165                 170                 175

Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
            180                 185                 190

Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile
```

```
                195                    200                    205

    Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu Tyr Arg Ser Phe Gly Gln
        210             215             220

    Gly Thr Lys Val Glu Ile Lys Arg Leu Glu Gly Gly Ser Glu Val
    225             230             235             240

    Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu
                245             250             255

    Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Thr Thr Tyr Trp Met
                260             265             270

    Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu
                275             280             285

    Ile His Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp
        290             295             300

    Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe Leu Gln
    305             310             315             320

    Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Ser
                325             330             335

    Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Pro
                340             345             350

    Val Thr Val Ser Val Asp His His His His His
        355             360
```

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<210> 12
<211> 358
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric sequence from multiple species

<400> 12
Met Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1               5               10              15


Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr
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```
                 20                      25                      30

    Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
         35                  40                  45


    Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser
         50                  55                  60


    Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln
    65                  70                  75                  80


    Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu Tyr Arg
                     85                  90                  95


    Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gln
                 100                 105                 110


    Phe Met Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro
             115                 120                 125


    Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Thr
         130                 135                 140


    Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
    145                 150                 155                 160


    Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro
                 165                 170                 175


    Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
                 180                 185                 190


    Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr
             195                 200                 205


    Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp Gly
         210                 215                 220


    Gln Gly Thr Pro Val Thr Val Ser Gly Gly Gly Ser Asp Ile Val
    225                 230                 235                 240


    Met Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Pro Gly Glu Arg Val
                 245                 250                 255
```

```
Thr Leu Thr Cys Lys Ser Ser Gln Ser Leu Phe Asn Ser Arg Thr Arg
            260                 265             270


Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
            275                 280             285


Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg
    290                 295             300


Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser
305             310             315                 320


Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Thr Gln Val Tyr Tyr
            325             330             335


Leu Cys Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Leu Asp
            340             345             350


His His His His His His
        355
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<210> 13
<211> 1152
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric sequence from multiple organisms

<400> 13
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gaagtgcagc tggtggagtc aggggagac ttagtgaagc tggagggtc cctgaaactc       120

tcctgtgcag cctctggatt cactttcagt atttacacca tgtcttggct tcgccagact      180

ccgggaaagg ggctggagtg ggtcgcaacc ctgagtggtg atggtgatga catctactat      240

ccagacagtg tgaagggtcg attcaccatc tccagagaca atgccaagaa cagcctatat      300

ctgcagatga cagtctaag ggctgaggac acggccttgt attactgtgc aagggtgcga       360

cttggggact gggacttcga tgtctgggc caagggacca cggtctccgt ctcctcagga       420

ggtggcggat ccgacatcca gctgacccag agcccaagca gcctgagcgc cagcgtgggt      480

gacagagtga ccatcacctg taaggccagt caggatgtgg gtacttctgt agcttggtac      540
```

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cagcagaagc caggtaaggc tccaaagctg ctgatctact ggacatccac ccggcacact      600

ggtgtgccaa gcagattcag cggtagcggt agcggtaccg acttcacctt caccatcagc      660

agcctccagc cagaggacat cgccacctac tactgccagc aatatagcct ctatcggtcg      720

ttcggccaag ggaccaaggt ggaaatcaaa cgtctcgagg gcggaggtag cgaggtccaa      780

ctggtggaga gcggtggagg tgttgtgcaa cctggccggt ccctgcgcct gtcctgctcc      840

gcatctggct tcgatttcac cacatattgg atgagttggg tgagacaggc acctggaaaa      900

ggtcttgagt ggattggaga aattcatcca gatagcagta cgattaacta tgcgccgtct      960

ctaaaggata gatttacaat atcgcgagac aacgccaaga acacattgtt cctgcaaatg     1020

gacagcctga gacccgaaga caccggggtc tattttgtg caagccttta cttcggcttc     1080

ccctggtttg cttattgggg ccaagggacc ccggtcaccg tctcagtcga ccatcatcat     1140

catcatcatt ga                                                         1152
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<210> 14
<211> 1134
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric sequence from multiple organisms

<400> 14
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gacatccagc tgacccagag cccaagcagc ctgagcgcca gcgtgggtga cagagtgacc      120

atcacctgta aggccagtca ggatgtgggt acttctgtag cctggtacca gcagaagcca      180

ggtaaggctc caaagctgct gatctactgg acatccaccc ggcacactgg tgtgccaagc      240

agattcagcg gtagcggtag cggtaccgac ttcaccttca ccatcagcag cctccagcca      300

gaggacatcg ccacctacta ctgccagcaa tatagcctct atcggtcgtt cggccaaggg      360

accaaggtgg aaatcaaacg tggaggtggc caattcatgg aggtccaact ggtggagagc      420

ggtggaggtg ttgtgcaacc tggccggtcc ctgcgcctgt cctgctccgc atctggcttc      480

gatttcacca catattggat gagttgggtg agacaggcac tggaaaagg tcttgagtgg      540

attggagaaa ttcatccaga tagcagtacg attaactatg cgccgtcgct aaaagataga      600

tttacaatat cgcgagacaa cgccaagaac acattgttcc tgcaaatgga cagcctgaga      660

cccgaagaca ccggggtcta ttttgtgca agcctttact tcggcttccc ctggtttgct      720

tattgggggcc aagggacccc ggtcaccgtc tccggaggcg tggatccga cattgtgatg      780
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acacaatctc catcctccct ggctgtgtca cccgggggaga gggtcactct gacctgcaaa      840

tccagtcaga gtctgttcaa cagtagaacc cgaaagaact acttgggttg gtaccagcag      900

aaaccagggc agtctcctaa acttctgatc tactgggcat ctactcggga atctggggtc      960

cctgatcgct tctcaggcag tggatccgga acagatttca ctctcaccat caacagtctg     1020

caggctgaag acgtggcagt ttattactgc actcaagttt attatctgtg cacgttcggt     1080

gctgggacca agctggagct gaaacggctc gaccatcatc atcatcatca ttga          1134
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<210> 15
<211> 9116
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric sequence from multiple organisms

<400> 15
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cgaaacccga caggactata aagataccag gcgtttcccc ctggaagctc cctcgtgcgc      120

tctcctgttc cgaccctgcc gcttaccgga tacctgtccg cctttctccc ttcgggaagc      180

gtggcgcttt ctcatagctc acgctgtagg tatctcagtt cggtgtaggt cgttcgctcc      240

aagctgggct gtgtgcacga accccccgtt cagcccgacc gctgcgcctt atccggtaac      300

tatcgtcttg agtccaaccc ggtaagacac gacttatcgc cactggcagc agccactggt      360

aacaggatta gcagagcgag gtatgtaggc ggtgctacag agttcttgaa gtggtggcct      420

aactacggct acactagaag gacagtattt ggtatctgcg ctctgctgaa gccagttacc      480

ttcggaaaaa gagttggtag ctcttgatcc ggcaaacaaa ccaccgctgg tagcggtggt      540

ttttttgttt gcaagcagca gattacgcgc agaaaaaaag gatctcaaga agatcctttg      600

atcttttcta cggggtctga cgctcagtgg aacgaaaact cacgttaagg gattttggtc      660

atgagattat caaaaaggat cttcacctag atccttttaa attaaaaatg aagttttaaa      720

tcaatctaaa gtatatatga gtaaacttgg tctgacagtt accaatgctt aatcagtgag      780

gcacctatct cagcgatctg tctatttcgt tcatccatag ttgcctgact ccccgtcgtg      840

tagataacta cgatacggga gggcttacca tctggcccca gtgctgcaat gataccgcga      900

gacccacgct caccggctcc agatttatca gcaataaacc agccagccgg aagggccgag      960

cgcagaagtg gtcctgcaac tttatccgcc tccatccagt ctattaattg ttgccgggaa     1020
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gctagagtaa gtagttcgcc agttaatagt ttgcgcaacg ttgttgccat tgctgcaggc   1080

atcgtggtgt cacgctcgtc gtttggtatg gcttcattca gctccggttc ccaacgatca   1140

aggcgagtta catgatcccc catgttgtgc aaaaaagcgg ttagctcctt cggtcctccg   1200

atcgttgtca gaagtaagtt ggccgcagtg ttatcactca tggttatggc agcactgcat   1260

aattctctta ctgtcatgcc atccgtaaga tgcttttctg tgactggtga gtactcaacc   1320

aagtcattct gagaatagtg tatgcggcga ccgagttgct cttgcccggc gtcaacacgg   1380

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gcacccaact gatcttcagc atcttttact ttcaccagcg tttctgggtg agcaaaaaca   1560

ggaaggcaaa atgccgcaaa aaagggaata agggcgacac ggaaatgttg aatactcata   1620

ctcttccttt ttcaatatta ttgaagcatt tatcagggtt attgtctcat gagcggatac   1680

atatttgaat gtatttagaa aaataaacaa ataggggttc cgcgcacatt tccccgaaaa   1740

ggccacctga cgtctaagaa accattatta tcatgacatt aacctataaa aataggcgta   1800

tcacgaggcc ctttcgtctt caagaattcc gatccagaca tgataagata cattgatgag   1860

tttggacaaa ccacaactag aatgcagtga aaaaaatgct ttatttgtga aatttgtgat   1920

gctattgctt tatttgtaac cattataagc tgcaataaac aagttaacaa caacaattgc   1980

attcatttta tgtttcaggt tcagggggag gtgtgggagg ttttttaaag caagtaaaac   2040

ctctacaaat gtggtatggc tgattatgat ctaaagccag caaaagtccc atggtcttat   2100

aaaaatgcat agctttagga ggggagcaga gaacttgaaa gcatcttcct gttagtcttt   2160

cttctcgtag acttcaaact tatacttgat gccttttcc tcctggacct cagagaggac    2220

gcctgggtat tctgggagaa gtttatattt ccccaaatca atttctggga aaaacgtgtc   2280

actttcaaat tcctgcatga tccttgtcac aaagagtctg aggtggcctg gttgattcat   2340

ggcttcctgg taaacagaac tgcctccgac tatccaaacc atgtctactt tacttgccaa   2400

ttccggttgt tcaataagtc ttaaggcatc atccaaactt ttggcaagaa aatgagctcc   2460

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